

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Marc G. ACHEN
Andrew F. WILKS
Steven A. STACKER
Kari ALITALO
- (ii) TITLE OF INVENTION: GROWTH FACTOR
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
 - (B) STREET: 1200 G Street, NW, Suite 700
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: United States of America
 - (F) ZIP: 20005
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: EVANS, Joseph D.
 - (B) REGISTRATION NO: 26,269
 - (C) REFERENCE/DOCKET NUMBER: 1064/42983
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 628-8800
 - (B) TELEFAX: (202) 628-8844
 - (C) TELEX: N/A

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2846 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (F) TISSUE TYPE: Human Breast
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAATTCAGT GAAGTAAGAA AGACAAAGTG TTCATTGGAG ATTTTAGTA AGGGGCCAAC	60
AGAGCTGCTA AAGTCATGCT TCACTTAACG ATGGGGATAT GTTCGGAGAA ATGCATTGTT	120
AGGTGATTTT GTCGTTGTGC AAGCATCTTA GAGTACACTT AGACAAACCT AGCTGGTATA	180
ACCTAGGTGT GTAGTAGGAT ATATGGTATA GCCTATTGTT CCTAGGCTAC AAACCCATAC	240

AGCATGTTCC TGTACTGAAT ACTGAGGCAA CTGCAACACC GTGGTGAGTA TTTGTGTATC	300
TAAACATACC TAAACATAGA AAAGATAACAG TAAAATATG GCATTATAGT CTTATGGGAC	360
TAATGTCATA CATACTGTC ATATATTGTT GACTGTGAA TGTTGACCTG AATGTCATTA	420
TGTGGCAGGC ACATGACTGT GTCGCTAACCC TTTGCACAAG ATTACTGTAG GATTACATGA	480
GATAGTTGTA AATAATTGGT GGGGTACTGG GCACCTAGTA GGTATGCATA CATGTTCAC	540
ATCATTATGG TTGTTTAAA TCACCTAACCC CAGGCCCTGC ACATAGTAAG ACATCAACAA	600
ATTGTAGCTG CTACTATTTT GCGCATCTAA TCTTAATATC ATTTATTTG TAGTCCTTGG	660
ATGTTCCCTC CTTTATGACT TCTTTTTTT TTGTTGTCCT TCCTTAGCC CTCCATCCTC	720
TACAGCTCAG CATCAGAACCA CTCTCTTTT AGACTCCGAT ATGGGGTCCCT CCAAGAAAGT	780
TACTCTCTCA GTGCTCAGCC GGGAGCAGTC GGAAGGGGTT GGAGCGAGGG TCCGGAGAAG	840
CATGGCAGA CCCGAGTTAA AAAATCTGGA TCCGTTTTA CTGTTGATG AATTAAAGG	900
AGGTAGACCA GGAGGATTTTC CTGATCATCC ACATCGAGGT TTTGAAACAG TATCCTACCT	960
CCTGGAAAGGG GGCAGCATGG CCCATGAAGA CTTCTGTGGA CACACTGGTA AAATGAACCC	1020
AGGAGATTTG CAGTGGATGA CTGCGGGCCG GGGCATTCTG CACGCTGAGA TGCCTTGCTC	1080
AGAGGAGCCA GCCCATGGCC TACAACGTG GGTTAATTTG AGGAGCTCAG AGAAGATGGT	1140
GGAGCCTCAG TACCAAGAAC TGAAAAGTGA AGAAATCCCT AAACCCAGTA AGGATGGTGT	1200
GACAGTTGCT GTCATTCTG GAGAAGCCCT GGGAAATAAG TCCAAGGTTT ACACTCGCAC	1260
ACCAACCTTA TATTTGGACT TCAAATTGGA CCCAGGAGCC AAACATTCCC AACCTATCCC	1320
TAAAGGGTGG ACAAGCTTCA TTTACACGAT ATCTGGAGAT GTGTATATTG CCCTCTCTAT	1380
ATCCCAGCAC AGGTATGCCAG AGGGCAGGGT GCCTTCAGC TTACAGAACCA TTCAGTGAGG	1440
GAAGAGAACATA TGAACACCAAG TCATGACACA TCCTGTGCAC AGATGAAAGT CCAGGCACCA	1500
TTATGTGTTT TGATACCTCG CTAAGACGTT GGCAACCTCC ATACTGATAA AGGGATGGAG	1560
CTACAGTGGGA CTCCAAGGGG AGCAGGAATC TGCCTATCTC CTGGGAGAAG GAAATGGAAG	1620
GAGGGCCCGA TGATGCACAA CAAAAAATAG AACCTCATCA CACAGCAGTG CTTGGAGAAG	1680
GTGACAGTGT CCAAGTGGAG ACAAGGGATC CCAAGAGAAG CCACTTGTC TTAATTGCTG	1740
GGGAGCCATT AAGAGAACCA GTTATCCAAC ATGCGATCAT CTCAGTCCAC ATTGGAACGA	1800
TCTGAACAGC AGATCAGGGC TGCTTCTAGT TTGGAGGAAC TACTTCGAAT TACTCACTCT	1860
GAGGACTGGGA AGCTGTGGAG ATGCAGGCTG AGGCTCAAA GTTTTACCAAG TATGGACTCT	1920
CGCTCAGCAT CCCATCGGTC CACTAGGTTT GCGGCAACTT TCTATGACAT TGAAACACTA	1980
AAAGTTATAG ATGAAGAACG GCAAAGAAC CAGTGCAGCC CTAGAGAAC GTGCGTGGAG	2040
GTGGCCAGTG AGCTGGGAA GAGTACCAAC ACATTCTTCA AGCCCCCTTG TGTGAACGTG	2100
TTCCGATGTG GTGGCTGTTG CAATGAAGAG AGCCTTATCT GTATGAACAC CAGCACCTCG	2160
TACATTTCCA AACAGCTCTT TGAGATATCA GTGCCTTGA CATCAGTACC TGAATTAGTG	2220
CCTGTTAAAG TTGCCAATCA TACAGGTTGT AAGTGCTTGC CAACAGCCCC CCGCCATCCA	2280

TACTCAATTA	TCAGAAGATC	CATCCAGATC	CCTGAAGAAG	ATCGCTGTT	CCATTCCAAG	2340
AAACTCTGTC	CTATTGACAT	GCTATGGGAT	AGCAACAAAT	GTAAAATGTGT	TTTGCAGGAG	2400
GAAAATCCAC	TCGCTGGAAC	AGAAGACCAC	TCTCATCTCC	AGGAACCAGC	TCTCTGTGGG	2460
CCACACATGA	TGTTTGACGA	AGATCGTTGC	GAGTGTGTCT	GTAAAACACC	ATGTCCCAA	2520
GATCTAATCC	AGCACCCAA	AAACTGCAGT	TGCTTGAGT	GCAAAGAAAG	TCTGGAGACC	2580
TGCTGCCAGA	AGCACAAGCT	ATTCACCCA	GACACCTGCA	GCTGTGAGGA	CAGATGCC	2640
TTTCATACCA	GACCATGTGC	AA GTGGCAA	ACAGCATGTG	CAAAGCATTG	CCGCTTTCCA	2700
AAGGAGAAAA	GGGCTGCCCA	GGGGCCCCAC	AGCCGAAAGA	ATCCTTGATT	CAGCGTTCCA	2760
AGTCCCCAT	CCCTGTCATT	TTAACAGCA	TGCTGTTTG	CCAAGTTGCT	GTCACTGTT	2820
TTTCCCAGG	TGTTAAAAAA	AAAAAA				2846

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro	Kaa	Cys	Val	Xaa	Xaa	Xaa	Arg	Cys	Kaa	Gly	Cys	Cys
1				5					10			

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (F) TISSUE TYPE: Human Breast

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Arg	Ser	Ser	Gln	Ser	Thr	Leu	Glu	Arg	Ser	Glu	Gln	Gln	Ile	Arg
1				5				10					15		

Ala	Ala	Ser	Ser	Leu	Glu	Glu	Leu	Leu	Arg	Ile	Thr	His	Ser	Glu	Asp
				20				25				30			

Trp	Lys	Leu	Trp	Arg	Cys	Arg	Leu	Arg	Leu	Lys	Ser	Phe	Thr	Ser	Met
			35			40					45				

Asp	Ser	Arg	Ser	Ala	Ser	His	Arg	Ser	Thr	Arg	Phe	Ala	Ala	Thr	Phe
			50			55				60					

Tyr Asp Ile Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr
 65 70 75 80
 Gln Cys Ser Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly
 85 90 95
 Lys Ser Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg
 100 105 110
 Cys Gly Gly Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser
 115 120 125
 Thr Ser Tyr Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr
 130 135 140
 Ser Val Pro Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys
 145 150 155 160
 Lys Cys Leu Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg
 165 170 175
 Ser Ile Gln Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu
 180 185 190
 Cys Pro Ile Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu
 195 200 205
 Gln Glu Glu Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln
 210 215 220
 Glu Pro Ala Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys
 225 230 235 240
 Glu Cys Val Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro
 245 250 255
 Lys Asn Cys Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys
 260 265 270
 Gln Lys His Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg
 275 280 285
 Cys Pro Phe His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala
 290 295 300
 Lys His Cys Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His
 305 310 315 320
 Ser Arg Lys Asn Pro
 325

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2029 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (F) TISSUE TYPE: Human Lung
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTTGGGTTCC AGCTTCTGT AGCTGTAAGC ATTGGTGGCC ACACCACCTC CTTACAAAGC	60
AACTAGAACCG CGGGCATAC ATTGGAGAGA TTTTTTAAT TTTCTGGACA TGAAGTAAAT	120
TTAGAGTGCT TTCTAATTTC AGGTAGAAGA CATGTCCACC TTCTGATTAT TTTTGGAGAA	180
CATTTGATT TTTTCATCT CTCTCTCCCC ACCCCTAAGA TTGTGAAAAA AAAGCGTACC	240
TTGCCTAATT GAAATAATT TGATCAGAAC TGATTATTG GTTTCTGTG	300
TGAAGTTTG AGGTTCAAA CTTTCCTCT GGAGAATGCC TTTTGAACAA ATTTCTCTA	360
GCTGCCTGAT GTCAACTGCT TAGTAATCAG TGGATATTGA AATATTCAAATGTACAGAG	420
AGTGGGTAGT GGTGAATGTT TTCATGATGT TGTACGTCCA GCTGGTGCAG GGCTCCAGTA	480
ATGAACATGG ACCAGTGAAG CGATCATCTC AGTCCACATT GGAACGATCT GAACAGCAGA	540
TCAGGGCTGC TTCTAGTTG GAGGAACCTAC TTCAATTAC TCACCTGAG GACTGGAAGC	600
TGTGGAGATG CAGGCTGAGG CTCAAAAGTT TTACCAAGTAT GGACTCTCGC TCAGCATCCC	660
ATCGGTCCAC TAGGTTGCG GCAACTTTCT ATGACATTGA AACACTAAAA GTTATAGATG	720
AAGAATGGCA AAGAACTCAG TGCAGCCCTA GAGAAACGTG CGTGGAGGTG GCCAGTGAGC	780
TGGGAAGAG TACCAACACA TTCTCAAGC CCCCTTGTGT GAAACGTGTTG CGATGTGGTG	840
GCTGTTGCAA TGAAGAGAGC CTTATCTGTA TGAACACCCAG CACCTCGTAC ATTTCAAAC	900
AGCTCTTGA GATATCAGTG CCTTGTACAT CAGTACCTGA ATTGTCGCT GTTAAAGTTG	960
CCAATCATAAC AGGTTGTAAG TGCTTGCCAA CAGCCCCCG CCATCCATAC TCAATTATCA	1020
GAAGATCCAT CCAGATCCCT GAAGAAGATC GCTGTTCCCA TTCCAAGAAA CTCTGTCCTA	1080
TTGACATGCT ATGGGATAGC AACAAATGTA AATGTGTTT GCAGGAGGAA AATCCACTTG	1140
CTGGAACAGA AGACCACTCT CATCTCCAGG AACCAAGCTCT CTGTGGGCCA CACATGATGT	1200
TTGACGAAGA TCGTTGCGAG TGTGTCTGTA AAACACCATG TCCCAAAGAT CTAATCCAGC	1260
ACCCAAAAAA CTGCAGTTGC TTTGAGTGCA AAGAAAGTCT GGAGACCTGC TGCCAGAAC	1320
ACAAGCTATT TCACCCAGAC ACCTGCAGCT GTGAGGACAG ATGCCCTTT CATACCAAGAC	1380
CATGTGCAAG TGGAAAACA GCATGTGCAA AGCATTGCCG CTTTCAAAG GAGAAAAGGG	1440
CTGCCAGGG GCCCCACAGC CGAAAGAAC CTTGATTCAAG CGTTCCAAGT TCCCCATCCC	1500
TGTCATTTT AAGCAGCATGC TGCTTGCCA AGTTGCTGTC ACTGTTTTT TCCCAGGTGT	1560
TAAAAAAAAA ATCCATTTA CACAGCACCA CAGTGAATCC AGACCAACCT TCCATTACACA	1620
CCAGCTAAGG AGTCCCTGGT TCATTGATGG ATGTCCTCTA GCTGCAGATG CCTCTGCGCA	1680
CCAAGGAATG GAGAGGAGGG GACCCATGTA ATCCTTTGT TTAGTTTGT TTTGTTTT	1740
TGGTGAATGA GAAAGGTGTG CTGGTCATGG AATGGCAGGT GTCATATGAC TGATTACTCA	1800
GAGCAGATGA GAAAAGTGT AGTCTCTGAG TCCTTGCTA ATCGCAACTC TTGTGAATTA	1860
TTCTGATTCT TTTTATGCA GAATTGATT CGTATGATCA GTACTGACTT TCTGATTACT	1920
GTCCAGCTTA TAGCTTCCA GTTAAATGAA CTACCATCTG ATGTTTCATA TTTAAGTGT	1980
TTTAAAGAAA ATAAACACCA TTATTCAAGC CAAAAAAA AAAAAAAA	2029

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 354 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(F) TISSUE TYPE: Human Lung

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Tyr	Arg	Glu	Trp	Val	Val	Val	Asn	Val	Phe	Met	Met	Leu	Tyr	Val
1					5				10					15	
Gln	Leu	Val	Gln	Gly	Ser	Ser	Asn	Glu	His	Gly	Pro	Val	Lys	Arg	Ser
					20			25					30		
Ser	Gln	Ser	Thr	Leu	Glu	Arg	Ser	Glu	Gln	Ile	Arg	Ala	Ala	Ser	
				35				40					45		
Ser	Leu	Glu	Glu	Leu	Leu	Arg	Ile	Thr	His	Ser	Glu	Asp	Trp	Lys	Leu
					50		55				60				
Trp	Arg	Cys	Arg	Leu	Arg	Leu	Lys	Ser	Phe	Thr	Ser	Met	Asp	Ser	Arg
					65		70			75				80	
Ser	Ala	Ser	His	Arg	Ser	Thr	Arg	Phe	Ala	Ala	Thr	Phe	Tyr	Asp	Ile
				85				90					95		
Glu	Thr	Leu	Lys	Val	Ile	Asp	Glu	Glu	Trp	Gln	Arg	Thr	Gln	Cys	Ser
				100				105					110		
Pro	Arg	Glu	Thr	Cys	Val	Glu	Val	Ala	Ser	Glu	Leu	Gly	Lys	Ser	Thr
					115		120				125				
Asn	Thr	Phe	Phe	Lys	Pro	Pro	Cys	Val	Asn	Val	Phe	Arg	Cys	Gly	Gly
				130			135				140				
Cys	Cys	Asn	Glu	Glu	Ser	Leu	Ile	Cys	Met	Asn	Thr	Ser	Thr	Ser	Tyr
					145		150			155				160	
Ile	Ser	Lys	Gln	Leu	Phe	Glu	Ile	Ser	Val	Pro	Leu	Thr	Ser	Val	Pro
					165			170			175				
Glu	Leu	Val	Pro	Val	Lys	Val	Ala	Asn	His	Thr	Gly	Cys	Lys	Cys	Leu
					180			185			190				
Pro	Thr	Ala	Pro	Arg	His	Pro	Tyr	Ser	Ile	Ile	Arg	Arg	Ser	Ile	Gln
					195		200				205				
Ile	Pro	Glu	Glu	Asp	Arg	Cys	Ser	His	Ser	Lys	Lys	Leu	Cys	Pro	Ile
					210		215				220				
Asp	Met	Leu	Trp	Asp	Ser	Asn	Lys	Cys	Lys	Cys	Val	Leu	Gln	Glu	Glu
					225		230			235				240	
Asn	Pro	Leu	Ala	Gly	Thr	Glu	Asp	His	Ser	His	Leu	Gln	Glu	Pro	Ala
					245				250				255		
Leu	Cys	Gly	Pro	His	Met	Met	Phe	Asp	Glu	Asp	Arg	Cys	Glu	Cys	Val
					260			265			270				

Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys
 275 280 285
 Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His
 290 295 300
 Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe
 305 310 315 320
 His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys
 325 330 335
 Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys
 340 345 350

Asn Pro

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (F) TISSUE TYPE: Mouse Lung

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGAGAATGCC	TTTGCAACA	CTTTCAAGTA	GCTGCCTGGA	AACAACTGCT	TAGTCATCGG	60
TAGACATTAA	AAATATTCAA	AATGTATGGA	GAATGGGAA	TGGGGATAT	CCTCATGATG	120
TTCCATGTGT	ACTTGGTGCA	GGGCTTCAGG	AGCGAACATG	GACCAGTGAA	GGATTTTCT	180
TTTGAGCGAT	CATCCCGTTC	CATGTTGGAA	CGATCTGAAC	AACAGATCCG	AGCAGCTTCT	240
AGTTTGGAGG	AGTTGCTGCA	AATCGCGCAC	TCTGAGGACT	GGAAGCTGTG	GCGATGCCGG	300
TTGAAGCTCA	AAAGTCTTGC	CAGTATGGAC	TCACGCTCAG	CATCCCCTCG	CTCCACCAGA	360
TTTGGCGCAA	CTTTCTATGA	CACTGAAACA	CTAAAAGTTA	TAGATGAAGA	ATGGCAGAGG	420
ACCCAATGCA	GCCCTAGAGA	GACATGCGTA	GAAGTCGCCA	GTGAGCTGGG	GAAGACAACC	480
AACACATTCT	TCAAGCCCCC	CTGTGTAAAT	GTCTTCCGGT	GTGGAGGCTG	CTGCAACGAA	540
GAGGGTGTGA	TGTGTATGAA	CACAAGCACC	TCCTACATCT	CCAAACAGCT	CTTTGAGATA	600
TCAGTGCCTC	TGACATCAGT	GCCCGAGTTA	GTGCCTGTTA	AAATTGCCAA	CCATACGGGT	660
TGTAAGTGCT	TGCCCCACGGG	CCCCCGCCAT	CCTTACTCAA	TTATCAGAAG	ATCCATTCA	720
ACCCCAGAAG	AAGATGAATG	TCCTCATTCC	AAGAAACTCT	GTCCTATTGA	CATGCTGTGG	780
GATAACACCA	AATGTAAATG	TGTTTGCAA	GACGAGACTC	CACTGCCTGG	GACAGAAGAC	840
CACTCTTACC	TCCAGGAACC	CACTCTCTGT	GGACCGCACA	TGACGTTGA	TGAAGATCGC	900
TGTGAGTGCG	TCTGTAAAGC	ACCATGTCCG	GGAGATCTCA	TTCAGCACCC	GGAAAACCTGC	960

AGTTGCTTG	AGTGCAAAGA	AAGTCTGGAG	AGCTGCTGCC	AAAAGCACAA	GATTTTCAC	1020
CCAGACACCT	GCAGCTGTGA	GGACAGATGT	CCTTTCA	CCAGAACATG	TGCAAGTAGA	1080
AAGCCAGCCT	GTGGAAAGCA	CTGGCGCTT	CCAAAGGAGA	CAAGGGCCA	GGGACTCTAC	1140
AGCCAGGAGA	ACCCTTGATT	CAACTTCCTT	TCAAGTCCCC	CCATCTCTGT	CATTTAAAC	1200
AGCTCACTGC	TTTGTCAAGT	TGCTGTCACT	GTTGCCACT	ACCCCTTGAA	CATGTGCAAA	1260
CACAGACACA	CACACACACA	CACACACAGA	GCAACTAGAA	TTATGTTTC	TAGGTGCTGC	1320
CTAAG						1325

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(F) TISSUE TYPE: Mouse Lung

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAACTTTGCT	TCTGGAGAAT	GCCTTTGCA	ACACTTTCA	GTAGCTGCCT	GGAAACAACT	60
GCTTAGTCAT	CGGTAGACAT	TTAAAATATT	CAAAATGTAT	GGAGAATGGG	GAATGGGAA	120
TATCCTCATG	ATGTTCCATG	TGTACTTGGT	GCAGGGCTTC	AGGAGCGAAC	ATGGACCAGT	180
GAAGCGATCA	TCCC GGTC	TGTTGGAACG	ATCTGAACAA	CAGATCCGAG	CAGCTTCTAG	240
TTTGGAGGAG	TTGCTGAAA	TCGCGCACTC	TGAGGACTGG	AAGCTGTGGC	GATGCCGGTT	300
GAAGCTCAAA	AGTCTTGCCA	GTATGGACTC	ACGCTCAGCA	TCCCATCGCT	CCACCCAGATT	360
TGCGGCAACT	TTCTATGACA	CTGAAACACT	AAAAGTTATA	GATGAAGAAT	GGCAGAGGAC	420
CCAATGCAGC	CCTAGAGAGA	CATGCGTAGA	AGTCGCCAGT	GAGCTGGGAA	AGACAAACCAA	480
CACATTCTTC	AAGCCCCCT	GTGTAAATGT	CTTCGGTGT	GGAGGCTGCT	GCAACGAAGA	540
GGGTGTGATG	TGTATGAACA	CAAGCACCTC	CTACATCTCC	AAACAGCTCT	TTGAGATATC	600
AGTGCCTCTG	ACATCAGTGC	CCGAGTTAGT	GCCTGTTAAA	ATTGCCAAC	ATACGGGTTG	660
TAAGTGCTTG	CCCACGGCC	CCCGCCATCC	TTACTCAATT	ATCAGAAAGAT	CCATTCAAGAC	720
CCCAGAAGAA	GATGAATGTC	CTCATTCCAA	GAAACTCTGT	CCTATTGACA	TGCTGTGGGA	780
TAACACCAAA	TGTAAATGTG	TTTGCAAGA	CGAGACTCCA	CTGCCTGGGA	CAGAAGACCA	840
CTCTTACCTC	CAGGAACCCA	CTCTCTGTGG	ACCGCACATG	ACGTTGATG	AAGATCGCTG	900
TGAGTGCCTC	TGTAAAGCAC	CATGTCCGGG	AGATCTCATT	CAGCACCCGG	AAAACGTGAG	960
TTGCTTGAG	TGCAAAGAAA	GTCTGGAGAG	CTGCTGCCAA	AAGCACAAAGA	TTTTTCACCC	1020
AGACACCTGC	AGGTCAATGG	TCTTTTCGCT	TTCCCCCTAA	CTTGGTTTAC	TGATGACATT	1080

TAAAGGACAT ACTAATCTGA TCTGTTCAAGG CTCTTTCTC TCAGAGTCCA AGCAC

1135

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(F) TISSUE TYPE: Mouse Lung

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Tyr Gly Glu Trp Gly Met Gly Asn Ile Leu Met Met Phe His Val
1 5 10 15

Tyr Leu Val Gln Gly Phe Arg Ser Glu His Gly Pro Val Lys Asp Phe
20 25 30

Ser Phe Glu Arg Ser Ser Arg Ser Met Leu Glu Arg Ser Glu Gln Gln
35 40 45

Ile Arg Ala Ala Ser Ser Leu Glu Leu Leu Gln Ile Ala His Ser
50 55 60

Glu Asp Trp Lys Leu Trp Arg Cys Arg Leu Lys Leu Lys Ser Leu Ala
65 70 75 80

Ser Met Asp Ser Arg Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala
85 90 95

Thr Phe Tyr Asp Thr Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln
100 105 110

Arg Thr Gln Cys Ser Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu
115 120 125

Leu Gly Lys Thr Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val
130 135 140

Phe Arg Cys Gly Gly Cys Cys Asn Glu Glu Gly Val Met Cys Met Asn
145 150 155 160

Thr Ser Thr Ser Tyr Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro
165 170 175

Leu Thr Ser Val Pro Glu Leu Val Pro Val Lys Ile Ala Asn His Thr
180 185 190

Gly Cys Lys Cys Leu Pro Thr Gly Pro Arg His Pro Tyr Ser Ile Ile
195 200 205

Arg Arg Ser Ile Gln Thr Pro Glu Glu Asp Glu Cys Pro His Ser Lys
210 215 220

Lys Leu Cys Pro Ile Asp Met Leu Trp Asp Asn Thr Lys Cys Lys Cys
225 230 235 240

Val Leu Gln Asp Glu Thr Pro Leu Pro Gly Thr Glu Asp His Ser Tyr
245 250 255

Leu Gln Glu Pro Thr Leu Cys Gly Pro His Met Thr Phe Asp Glu Asp
260 265 270

Arg Cys Glu Cys Val Cys Lys Ala Pro Cys Pro Gly Asp Leu Ile Gln
 275 280 285

His Pro Glu Asn Cys Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Ser
 290 295 300

Cys Cys Gln Lys His Lys Ile Phe His Pro Asp Thr Cys Ser Cys Glu
 305 310 315 320

Asp Arg Cys Pro Phe His Thr Arg Thr Cys Ala Ser Arg Lys Pro Ala
 325 330 335

Cys Gly Lys His Trp Arg Phe Pro Lys Glu Thr Arg Ala Gln Gly Leu
 340 345 350

Tyr Ser Gln Glu Asn Pro
 355

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (F) TISSUE TYPE: Mouse Lung

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Tyr Gly Glu Trp Gly Met Gly Asn Ile Leu Met Met Phe His Val
 1 5 10 15

Tyr Leu Val Gln Gly Phe Arg Ser Glu His Gly Pro Val Lys Arg Ser
 20 25 30

Ser Arg Ser Met Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
 35 40 45

Ser Leu Glu Glu Leu Leu Gln Ile Ala His Ser Glu Asp Trp Lys Leu
 50 55 60

Trp Arg Cys Arg Leu Lys Leu Lys Ser Leu Ala Ser Met Asp Ser Arg
 65 70 75 80

Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Thr
 85 90 95

Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
 100 105 110

Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Thr Thr
 115 120 125

Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
 130 135 140

Cys Cys Asn Glu Glu Gly Val Met Cys Met Asn Thr Ser Thr Ser Tyr
 145 150 155 160

Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
 165 170 175

Glu Leu Val Pro Val Lys Ile Ala Asn His Thr Gly Cys Lys Cys Leu
180 185 190

Pro Thr Gly Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
195 200 205

Thr Pro Glu Glu Asp Glu Cys Pro His Ser Lys Lys Leu Cys Pro Ile
210 215 220

Asp Met Leu Trp Asp Asn Thr Lys Cys Lys Cys Val Leu Gln Asp Glu
225 230 235 240

Thr Pro Leu Pro Gly Thr Glu Asp His Ser Tyr Leu Gln Glu Pro Thr
245 250 255

Leu Cys Gly Pro His Met Thr Phe Asp Glu Asp Arg Cys Glu Cys Val
260 265 270

Cys Lys Ala Pro Cys Pro Gly Asp Leu Ile Gln His Pro Glu Asn Cys
275 280 285

Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Ser Cys Cys Gln Lys His
290 295 300

Lys Ile Phe His Pro Asp Thr Cys Arg Ser Met Val Phe Ser Leu Ser
305 310 315 320

Pro

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (vi) ORIGINAL SOURCE:
 - (F) TISSUE TYPE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGCTGCTTC TAGTTGGAG 20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (vi) ORIGINAL SOURCE:
 - (F) TISSUE TYPE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CACTCGCAAC GATCTTCGTC 20